

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 17, 2003, 08:44:41 ; Search time 13 Seconds
(without alignments)
2482.199 Million cell updates/sec

Title: US-10-010-227-3
Perfect score: 4055
Sequence: 1 MGAESTPQTLVDKVLQAHV.....KAVPVPTNRGEEKPELEW 778

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2682.5	66.2	755	1 LEU2_RH1PU	P55251 rhizomucor
2	2546	62.8	750	1 LEU2_RH1NI	P55811 rhizopus ni
3	2543	62.7	744	1 LEU2_PHYBL	P18250 phycomyces
4	2492.5	61.5	773	1 LEU2_US7MA	P49601 us7illago ma
5	2473.5	61.0	758	1 LEU2_SCHPO	O14289 schizosacch
6	2456.5	60.6	779	1 LEU2_YEAST	P07266 saccharomyc
7	2417.5	59.6	770	1 LEU2_CANMA	O00464 candida mal
8	2076	51.2	764	1 LEU2_RH1RA	P17279 rhizomucor
9	1636	40.3	469	1 LEU2_RH1ME	O92176 rhizobium m
10	1611	39.7	469	1 LEU2_BR1ME	O91769 bruceella me
11	1584	39.1	469	1 LEU2_AGR75	O8ub9 agrbacteria
12	1567.5	38.7	469	1 LEU2_RH1LO	O98ef1 rhizobium l
13	1562	38.5	479	1 LEU2_CANCR	O9abno caulobacter
14	1548.5	38.2	469	1 LEU2_NE1MB	O9jz15 neisseria m
15	1545.5	38.1	469	1 LEU2_NE1MA	O9jue2 neisseria m
16	1522.5	37.5	479	1 LEU2_XANCP	P58949 xanthomonas
17	1514.5	37.3	479	1 LEU2_XANAC	O9hz48 xanthomonas
18	1507.5	37.2	474	1 LEU2_PSEAE	O9hz43 pseudomonas
19	1498.5	37.0	474	1 LEU2_XYLFA	O9pax0 xyliella fas
20	1493	36.8	469	1 LEU2_RALSO	O9pax0 xyliella fas
21	1483.5	36.6	465	1 LEU2_ECOLI	P30127 escherichia s
22	1477.5	36.4	465	1 LEU2_SALTY	P15717 salmonella
23	1477.5	36.4	465	1 LEU2_SALTY	O82912 salmonella
24	1471	36.3	468	1 LEU2_HA1IN	P49668 haemophilus
25	1469.5	36.2	465	1 LEU2_ECO57	O8xao0 escherichia
26	1452	35.8	476	1 LEU2_YERPE	O8zi10 yerersinia pe
27	1446.5	35.7	467	1 LEU2_PASMU	O9Cjnr pasteurella
28	1425.5	35.2	467	1 LEU2_VIBCH	O9kp81 vibrio chol
29	1413	34.8	485	1 LEU2_ACTTI	O44427 actinoplan
30	1399.5	34.5	471	1 LEU2_BUCAI	P56934 buchnera ap
31	1396	34.4	472	1 LEU2_BACHD	O9k8f0 bacillus ha
32	1393.5	34.4	472	1 LEU2_BACSU	P80850 bacillus su
33	1385.5	34.2	476	1 LEU2_STRCO	O86534 streptomyce

34	1385	34.2	473	1 LEU2_MYCTU	O53237 mycobacteri
35	1354.5	33.4	466	1 LEU2_BUCDN	O85072 buchnera ap
36	1354	33.4	469	1 LEU2_BUCAP	O85065 buchnera ap
37	1354	33.4	476	1 LEU2_MYCLE	O31123 mycobacteri
38	1347.5	33.2	481	1 LEU2_CORGL	P58916 corynebacte
39	1330	32.8	471	1 LEU2_BUCRP	P48573 buchnera ap
40	1322.5	32.6	465	1 LEU2_BUCPS	P58945 buchnera ap
41	1311.5	32.3	470	1 LEU2_CAMJE	O9p1w1 campylobact
42	1290.5	31.8	466	1 LEU2_BUCTS	O31293 buchnera ap
43	1283.5	31.7	462	1 LEU2_LISIN	O92426 listeria in
44	1282	31.6	456	1 LEU2_STRAM	O99813 staphylococ
45	1281	31.6	456	1 LEU2_STPAM	P58947 staphylococ
46	1279.5	31.6	462	1 LEU2_LISMO	O8y517 listeria mo
47	1278.5	31.5	444	1 LEU2_BUCUM	O9ev98 buchnera ap
48	1275.5	31.5	443	1 LEU2_BUCUE	O9ev98 buchnera ap
49	1259.5	31.1	443	1 LEU2_BUCUA	O9ev95 buchnera ap
50	1253.5	30.9	443	1 LEU2_BUCUN	O9ev16 buchnera ap
51	1252.5	30.9	442	1 LEU2_BUCUS	O9ev13 buchnera ap
52	1236.5	30.5	443	1 LEU2_BUCUE	O9evh4 buchnera ap
53	1227.5	30.2	442	1 LEU2_BUCUD	O9evh7 buchnera ap
54	1225.5	30.2	444	1 LEU2_BUCUD	O9ev0 buchnera ap
55	1217.5	30.0	473	1 LEU2_SALTY	O8zj10 salmonella
56	1211.5	29.9	442	1 LEU2_BUCML	O9ev92 buchnera ap
57	1209.5	29.8	472	1 LEU2_THERT	O9znd5 thermus the
58	1194.5	29.5	456	1 LEU2_STRGN	O9atm3 streptococc
59	1181.5	29.1	468	1 LEU2_SYNY3	P54384 synecocyst
60	1172.5	28.9	467	1 LEU2_ANASP	O8yx02 anabaena sp
61	1133.5	27.9	460	1 LEU2_LACLA	O02142 lactococcus
62	1066	26.3	470	1 LEU2_AZOVI	P96195 azotobacter
63	1065.5	26.3	369	1 LEU2_BUCUL	O9aq6 buchnera ap
64	699.5	17.3	418	1 LEU2_METXA	O8v1f2 methanopyru
65	684.5	16.9	432	1 LEU2_AQUAE	O67078 aquiflex aeo
66	662.5	16.3	267	1 LEU2_ALCEU	O44023 alcaligenes
67	660	16.3	424	1 LEU2_METAC	O81f1 methanocarc
68	656.5	16.2	424	1 LEU2_PYRRU	O8u2a1 pyrococcus
69	641	15.8	431	1 LEU2_DHIRA	O9ic16 deinococcus
70	637.5	15.7	423	1 LEU2_PYRAB	O9u207 pyrococcus
71	635	15.7	424	1 LEU2_METXA	P81292 methanococ
72	627.5	15.5	174	1 LEU2_RH1ET	O8vna6 rhizobium e
73	613	15.1	419	1 LEU2_METTH	O81f1 methanocarc
74	602.5	14.9	420	1 LEU2_METUA	O58409 methanococ
75	595.5	14.7	417	1 LEU2_THEMA	O9w224 thermotoga
76	587.5	14.5	418	1 LEU2_ARCFU	O28316 archaeoglob
77	584.5	14.4	775	1 LEU4_EMENT	O92412 emericeella
78	576.5	14.2	422	1 LEU2_CLOAB	O976h0 clostridium
79	573.5	14.1	416	1 LEU2_ARCFU	O28084 archaeoglob
80	562	13.9	420	1 LEU2_METAC	O8tq23 methanosarc
81	552	13.6	428	1 LEU2_METTH	O27668 methanobact
82	541.5	13.4	418	1 LEU2_THEMA	O9wyc7 thermotoga
83	539	13.3	215	1 LEUD_AZOVI	P49367 azotobacter
84	533.5	13.1	693	1 LEY4_YEAST	P96196 saccharomyc
85	523.5	12.9	418	1 LEU2_THERT	O9zne0 thermus the
86	512	12.6	434	1 LEU2_DHIRA	O9ry9 deinococcus
87	511.5	12.6	418	1 LEU2_THERT	O8ic92 thermoaer
88	505	12.5	201	1 LEUD_SALTY	P04787 salmonella
89	495	12.2	200	1 LEUD_HA1IN	P44383 haemophilus
90	491	12.1	201	1 LEUD_ECOLI	P30126 escherichia
91	482.5	11.9	191	1 LEUD_LACLA	O02144 lactococcus
92	482.5	11.9	780	1 ACQN_HUMAN	O99798 homo sapien
93	475	11.7	777	1 ACQN_CAEBL	P34455 caenorhabdi
94	466.5	11.5	199	1 LEUD_BACSU	P94568 bacillus su
95	462.5	11.4	781	1 ACQN_PIG	P16276 sus scrofa
96	454.5	11.2	780	1 ACQN_BOVIN	P20004 bos taurus
97	447	11.0	415	1 LEU2_PYRAE	O9zxx41 pyrobaculum
98	444.5	11.0	789	1 ACQN_YEAST	P39933 saccharomyc
99	443.5	10.9	779	1 ACQN_GRAVB	P49609 graciilaria
100	441	10.9	402	1 LEU2_METXA	O8tw29 methanopyru

ALIGNMENTS

RESULT 1

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LEU2_RHIPU
ID LEU2_RHIPU STANDARD; PRT; 755 AA.
AC P55251;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-isopropylmalate dehydratase (EC 4.2.1.33) (Isopropylmalate
isomerase) (Alpha-IPM isomerase) (IPMI).
GN LEUA.
OS Rhizomucor pusillus.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC Rhizomucor.
OX NCBI_TaxID=4840;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96339000; PubMed=8766701;
RA Wada M., Beppu T., Horiuchi S.;
RT "Integrative transformation of the zygomycete Rhizomucor pusillus by
homologous recombination.";
RL Appl. Microbiol. Biotechnol. 45:652-657(1996).
CC -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
H(2)O.
CC -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
isopropylmalate.
CC -!- PATHWAY: Leucine biosynthesis; second step.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
CC
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QY 189 GVSKDQVVLHAIIGIITAGGTGAVIERGSGVIRSLSMEARMSICNMSIEGGARAGWAPD 248
DB 183 GVTSKDQVILHIIIGVITAGGTGCVIEFCGSAFQMSMARMSVCNMSIEAGARAGMIAPD 242
QY 249 EITFEYLKGRPLAPKYDSPWHKATQYWKNIQSDPGAKYDIDVDFIDAKDIDVPTLTWTGSP 308
DB 243 EITFEYIRGRPLAP--TGAEDWKAVEYWRSLRSDPAKYDVDVDFIDADAIAPTLTWTGSP 300
QY 309 EDVVPITGVVPPDPETFAATEAKKADGRMLQYMGILKAGTFPMEDIIPVDKVFISGTSNRIED 368
DB 301 QDVVAITGTTTDPSTVSDPIRRQAMERALDYIGLKPNTPMQEVKIDKVFISGTSNRIED 360
QY 369 LRAAAAIVVKGKKAPNVKSMVPGSGVLVKTQABEEGLDKIFEAEAGFWRREAGCSMCLGM 428
DB 361 LRAAAAIAKGRHVADWV-YAMVVPVPGSLVKKQABEQEGLDRIFKEAGFDWREAGCSMCLGM 419
QY 429 NPDILAPQERCASTSNRNFEGROGAGGRTHLMSVPMAAAAGIVGKLADVRKLT----DYK 484
DB 420 NPDOLKEGRCASISNRNFEGROGAGGRTHLMSVPMAAAAGIVGKLADVRKLTQAQDRP 479
QY 485 ASPHIAAYQKSTVTKPHVDERINDOAHKDIIDIPEDNNGPHNTTSASVGTSAGLPKPT 544
DB 480 ASP--TPKKIETELEPPVEDHA-KAADQADIVTDAPATGASP---PSPAPSDAAGMPKPT 533
QY 545 ILKGIAAPLEKANYVTDALIPKQFLKTKRTGLGNALFVEMREN-EDGTEKSDFLVINKEP 603
DB 534 TLRGYAAPLDIANVYDTMIIPKQFLKTKRTGLGTLALFYNIRFDGATGEENPDFVLNQEP 593
QY 604 YRKASILLVCTGANFGCGSSREHAPWALNDFGIRSVIAPSFADIFFNNSFKNGMLPIPKD 663
DB 594 YRQSRILLVCTGPNFGCGSSREHAPWAFNDFGIRSVIAPSFADIFFNNSFKNGMLPITL-P 652
QY 664 QAOIEATAAARAKIEVDLPNQLIKNATGETICTTFFVEPRKXCLVNLGDDIGLTMQM 723
DB 653 QDKVEMLAHAQKAELEVDLVNVVRYPGGEV--PFDVEPRKXCLVNLGDDIGLTMQM 710
QY 724 EDKTAIEAKWTRTPMLDGVLYLKRKGQGLAKAAKVPVPTTNRGEEKKEPLEW 778
DB 711 ADLIEAFEARKSQTWPLMDGKDY-----AGK-ATKFTPVATNT---AKKQKLDW 755
RESULT 2
LEU2_RHINI
ID LEU2_RHINI STANDARD; PRT; 750 AA.
AC P55811;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-isopropylmalate dehydratase (EC 4.2.1.33) (Isopropylmalate
isomerase) (Alpha-IPM isomerase) (IPMI).
GN LEU1.
OS Rhizopus niveus.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC Rhizopus.
OX NCBI_TaxID=4844;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Yamazaki / IFO 4810;
RX MEDLINE=97056764; PubMed=8901103;
RA Takaya N., Yanai K., Horiuchi H., Ohta A., Takagi M.;
RT "Cloning and characterization of the Rhizopus niveus leul gene and
its use for homologous transformation.";
RL Biosci. Biotechnol. Biochem. 60:448-452(1996).
CC -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
H(2)O.
CC -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
isopropylmaleate.
CC -!- PATHWAY: Leucine biosynthesis; second step.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
CC

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DR	PIR;	\$10998;	\$109
DP	PTP;	\$26864;	\$268

DR PIR; S26864; S26864.

RESULT 4
LEU2_USTMA STANDARD; PRT; 773 AA.
ID LEU2_USTMA
AC P49601;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-isopropylmaleate dehydratase [EC 4.2.1.33] (Isopropylmaleate isomerase) (Alpha-IPM isomerase) (IPMI).
DE LEU1.
OS Ustilago maydis (Smut fungus).
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=5270;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94171070; PubMed=8125330;
RX Rubin B.P., Li D., Holloman W.K.;
RT "The LEU1 gene of Ustilago maydis.";
RL Gene 140:131-135(1994).
CC -! FUNCTION: Catalyzes the isomerization between 2-isopropylmaleate and 3-isopropylmaleate, via the formation of 2-isopropylmaleate.
CC -! CATALYTIC ACTIVITY: 3-isopropylmaleate = 2-isopropylmaleate + H(2O).
CC -! CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2O) = 2-isopropylmaleate.
CC -! PATHWAY: Leucine biosynthesis; second step.
CC -! SUBUNIT: Monomer (By similarity).
CC -! SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
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DR EMBL; L20832; AAA34226.1; -
DR InterPro; IPR000573; Aconitase_C.
DR InterPro; IPR001030; Aconitase_N.
DR InterPro; IPR004430; LeuC.
DR InterPro; IPR004431; LeuD.
DR Pfam; PF00330; aconitase; 1.
DR Pfam; PF00694; Aconitase_C; 1.
DR PRINTS; PR00415; ACONITASE.
DR ProDom; PD000511; Aconitase_N; 1.
DR TIGRFAMs; TIGR00170; leuC; 1.
DR TIGRFAMs; TIGR00171; leuD; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
DR Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.
KW METAL 355 355 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT FT METAL 415 415 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT FT METAL 418 418 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 773 AA; 83224 MW; A936D8D1990DDC1C CRC64;
Query Match 61.5%; Score 2492.5; DB 1; Length 773;
Best Local Similarity 64.0%; Pred. No. 9 4e-161;
Matches 488; Conservative 92; Mismatches 142; Indels 41; Gaps 9;
QY 8 POTLDKVLQAHVVDKLGDTVLLYIDRHVHEVTSPOAFEGLRNAGRKVRPDCLTATT 67
Db 3 PKTLVEKIIFDSHLVHEADGTCIYIDRHVHEVTSPOAFEGLRNANRVRRDCTLATV 62
QY 68 DHNVPTTSKALKDIASFTEKEDSDRSTQCVTILEENVKEFGTVTFGLSKRGIVHVGPEQ 127
Db 63 DHNIPTASKRSVRDTSKFVEQVDSRTQCMTLEENVKAFGLTFPGLSDNQRQGIHHIGPEQ 122
QY 128 GTFLPQTTVVCDSHTSTHGAFGALAFGIGTSEVHEVLATQCLITKRKNMRIQVDGELA 187

Db 123 GFTLPGATVCGSDHSTHTGAFGALAFGICTSEVHVLATQTLQKRAKMLIQVDELS 182
 Qy 188 PGVSSKDVVLAIGITAGTGAIVIEFCGSVIRLSMEARMSICNMSIEGARAGVAP 247
 Db 183 QGVTSKDIIHIIIGLIGTAGTGVIVIEFAGSTIRLSMEARMSICNMSIEGARAGIAP 242
 Qy 248 DEITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIPVTLWTGS 307
 Db 243 DEITFEYIKRPLAPK-QGBAMQDALVWKMTLPBDEGAQYDVTVIKIDAKDIPVTVWTS 301
 Qy 308 PEDVPTGTGVPPPETATATAKADGRMLQYMKLAKGTPEMDIPVUKVFSGSTNRIE 367
 Db 302 PDVVVATGTVPPEPKASNAEAKAWTRALEYMWLEAGTPEMKIKIDKVFISGCTNARIE 361
 Qy 368 DLAAAAVAVGRKAPVAVKAMVPGSGLVTKQAESEGLDKIFEEAGFEMREACSCMCLG 427
 Db 362 DLRAAAAVLGRKAYADL-YCMLVPGSGLVTKQAEAGLDKIFPAAGFDMREACSCMCLG 420
 Qy 428 MNPDIAPPOERCASSTNSRNFEGRQAGGRTHLMSPVMAAAGIVGLADVRKLTGYKASP 487
 Db 421 MNPDIAPPOERCASSTNSRNFEGRQAGGRTHLMSPVMAAAGIVGLADVRKLVG- 475
 Qy 488 HIAAYQKSTYTKPHVDRIQD-----DA-----HEKDIADIPEDNN 524
 Db 476 HSSAKVGSDAKAPFAFEIVSDAKSYLVADATPPAPATVVAAGALTDDEALRDVP--- 531
 Qy 525 GPHNTASVGTSGAGLKPFTLKIGIAPLEKAVDTDAIIPKQFLTKTKTGKGNALFYE 584
 Db 532 ASHSSS-----GGMKKFTTLTGIAAPLEKSNVDTDIIIPKQFLTKTKTGKGNALFWE 586
 Qy 585 MRFN-EDGTERKSDPVLNKEPYRKASIIIVCTGANFGCGSSREHAPWALNDFGIRSVIAPSF 643
 Db 587 LRDAKATGEPDPAPVLAQKPYDQSKIIIVTGPNGCGSSREHAPWALNDFGIRSVIAPSF 646
 Qy 644 ADIFPNNSFKKMLPIPIKQAOIEAIAEAPAKETIEVDIPNOLIKATGETICTPEVE 703
 Db 647 GDIFRNMLTKNGQLPV-VLSRAQIQRLODPAKAKQIIVDVLVDLVTADKKEKESFETP 705
 Qy 704 EFRHCHVNGLDIDGLTQMOMEDKIAEFPKAKWTRENPMLDGTGY 746
 Db 706 EFRHCHVNGLDIDGLTQMOMEDKIAEFPKAKWTRENPMLDGTGY 748
 RESULT 5
 LEU2_SCHPO STANDARD; PRT: 758 AA.
 ID LEU2_SCHPO STANDARD; PRT: 758 AA.
 OI4289;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 3-isopropylmalate dehydratase (EC 4.2.1.33) (isopropylmalate
 de isomerase) (Alpha-IPM isomerase) (IPMI).
 OS Schizosaccharomyces pombe (Fission yeast).
 ON Schizosaccharomyces pombe.
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 NCBI_TaxID=4896;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Scourto J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitz E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodard J., Volckaert G., Aert R., Robben J., Gymnopoulos B.,
 RA Welfjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Mambrot R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
 RA Smpakovski G.V., Usery D., Barrell B.G., Nurse P.,
 RL "The genome sequence of Schizosaccharomyces pombe."
 RT Nature 415:871-880(2002).
 CC - FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
 and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
 CC - CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
 H(2)O.
 CC - CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
 CC isopropylmalate.
 CC - PATHWAY: Leucine biosynthesis; second step.
 CC - SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: 299262; CABL6402.1; -.
 DR InterPro: IPR000573; Aconitase_C.
 DR InterPro: IPR001030; Aconitase_N.
 DR InterPro: IPR004430; Leuc.
 DR InterPro: IPR004430; Leuc.
 DR Pfam: PF00330; aconitase; 1.
 DR Pfam: PF00694; Aconitase_C; 1.
 DR PRINTS: PR00415; ACONITASE.
 DR Prodom: PD000511; Aconitase_N; 1.
 DR TIGRFAMs: TIGR00170; leuc; 1.
 DR TIGRFAMs: TIGR00171; leuc; 1.
 DR PROSITE: PS00450; ACONITASE_1; 1.
 DR PROSITE: PS01244; ACONITASE_2; 1.
 KW Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.
 FT METAL 359 359
 FT METAL 420 420
 FT METAL 423 423
 FT METAL IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 SQ SEQUENCE 758 AA; 82782 MW; CE78C36828380E47 CRC64;
 Query Match 61.0%; Score 2473.5; DB 1; Length 758;
 Best Local Similarity 62.9%; Pred. No. 1.8e-159;
 Matches 489; Conservative 92; Mismatches 172; Indels 25; Gaps 9;
 Qy 1 MPGASPTQTLVDYKVLQAVVDEKIDGTVLLYIDRLVHEVTSPOAFGLRNAGKVRP 60
 Db 1 MSPVASPKTLVDKWKVSHVVDLQEDGTCLLYIDRLVHEVTSPOAFGLRTAGKVRHP 60
 Qy 61 DCTLATDHNVTTSRKALKLTIASFIXEDDSRTQCVTLSENVKRGVYFPLGSDRQGITV 120
 Db 61 ELALATVDHNIPIDPRKMKKIASFIHOPDSRTQVLALENNIKKGLTYVMNDRQGITV 120
 Qy 121 HVIGPEGFTLPGTTVVGSDHSTHTGAFGALAFGICTSEVHVLATQCLTKRSKNMRI 180
 Db 121 HVIGPEGFTLPGTTVVGSDHSTHTGAFGALAFGICTSEVHVLATQCLTKRSKNMRI 180
 Qy 181 QVDEGLAPVSSKDVVLAIGITAGTGAIVIEFCGSVIRLSMEARMSICNMSIEGGA 240
 Db 181 RVNGKLPGIASKDLIIHIIIGITAGTGAIVIEFCGSAIEGLSWEARMSICNMSIEGGA 240
 Qy 241 RAGVAPDEITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDVP 300

```
Db 241 RAGMIADPATTFFVVKVRPLAPKGD--DWEQAVYWKTLRSDENAKYDIEVEINAADVLP 298
Qy 301 TLWTGSPEDVPITGVVPPDETEATEAKKADGRMLQYMLKAGTTPMEDIPVDKVFIFGS 360
Db 299 TVTWTGSPQDVPINGNI PDPAHVKDNRASIORSLLEYMGLKNTSVISVPIDKVFIFGS 358
Qy 361 CTNSRIEDLRAAAVVKGRKAPNVKAMVPGSLVKTQAEGLDKIFEEAGFEWREA 420
Db 359 CTNSRIEDLRAAAVVKGRKAPNVKAMVPGSLVKTQAEGLDKIFEEAGFEWREA 418
Qy 421 GCSMCLGMNPDILAPQERCASTSNRNEGOGAGRTHLMSVMAAAGIVGKLADVRKL 480
Db 419 GCSMCLGMNPDQLPYERCASTSNRNEGOGAGRTHLMSVMAAAGIVGKLADVRKL 478
Qy 481 TDYKASPHIAAYQKSTVTKPHVDERINQDAH--EKDIADIPEDNNGPHNTSASVGT- 536
Db 479 FG-----DVNSGSPSIITKNYDPSHDVEGDIGLSVDATDAVTDAGIATNAGSVSSG 533
Qy 537 SAGLPKFTILKGAAPLEKANVDTDAIIPKQFLTKIKRTGLGNALFYEMRNFNEDGTEKSD 596
Db 534 SAGIPKFTVVEGIAAPLPMAVDTDKIIPKQFLTKIKRTGLGNALFYEMRNFNEDGTEKSD 593
Qy 597 FVLNKEPYRKASITLVCTGANFGGSSREHAPWALNDFGIRSVIAPSPADIFPNNSFKNGM 656
Db 594 FVLNKEPYRKATVLAHD--NFGGSSREHAPWALNDFGIRSVIAPSPADIFPNNSFKNGM 652
Qy 657 LPIPIKDAQIEAIAEAPARAKEIEVDLPNQLIKNATGETICTEVEBEFRKHCLVNGLDD 716
Db 653 LPIPTPIE-QVNDMMKAENQVFSVDLVNQTI--TVGDKQVKEDVEFRKHCLVNGLDD 709
Qy 717 IGLTMQMEDKIAPEAKWTRTETWLDGTGVLKRGQGGKLAAKAVPVPTNRRGEKKE 774
Db 710 IGLTLQKETTIDAFEAAREENFFPMN-----IKRS-----RARLSPVKSNKQSSSRND 757

RESULT 6
LEU2_YEAST STANDARD; PRT; 779 AA.
AC P07264;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-isopropylmalate dehydratase (EC 4.2.1.33) (Isopropylmalate
DE isomerase) (Alpha-IPM isomerase) (IPMI).
GN LEU1 OR YGL009C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL125-2B;
RX MEDLINE=91353082; PubMed=1840714;
RA Skala J., Capieaux E., Balzi E., Chen W., Goffeau A.;
RT "Complete sequence of the Saccharomyces cerevisiae LEU1 gene encoding
RT isopropylmalate isomerase.";
RL Yeast 7:281-285 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Hebling U., Hofmann B., Delius H.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-48 FROM N.A.
RX MEDLINE=84162042; PubMed=6323436;
RA Hsu Y.-P., Schimmel P.R.;
RT "Yeast LEU1. Repression of mRNA levels by leucine and relationship of
RT 5'-noncoding region to that of LEU2.";
RL J. Biol. Chem. 259:3714-3719 (1984).
RN [4]
RP SEQUENCE OF 740-779 FROM N.A.
RC STRAIN=IL125-2B;
RX MEDLINE=91353083; PubMed=1882553;
RA Chen W., Balzi E., Capieaux E., Choder M., Goffeau A.;
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RT RT
RT RT
RT RT
RL Yeast 7:287-299 (1991).
CC -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC -!- CATALYTIC ACTIVITY: 3-isopropylmaleate = 2-isopropylmaleate +
CC H(2)O.
CC -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC isopropylmaleate.
CC -!- PATHWAY: Leucine biosynthesis; second step.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
CC
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CC
CC -----
CC EMBL; S57886; AAB19612.1; -.
CC EMBL; 272531; CAA96709.1; -.
CC EMBL; K01969; AAA34742.1; -.
CC EMBL; S58126; CAB31643.1; -.
CC PIR; A24105; A24105.
CC PIR; S15039; S15039.
CC PIR; S31555; S31555.
CC SGD; S0002977; LEU1.
CC
CC InterPro; IPR000573; Aconitase C.
CC InterPro; IPR001030; Aconitase_N.
CC InterPro; IPR004430; LeuC.
CC InterPro; IPR004431; LeuD.
CC Pfam; PF00330; aconitase; 1.
CC Pfam; PF00694; Aconitase_C; 1.
CC PRINTS; PR00415; ACONITASE.
CC PRODOM; PD000511; Aconitase_N; 1.
CC TIGRFAMs; TIGR00170; leuC; 1.
CC TIGRFAMs; TIGR00171; leuD; 1.
CC PROSITE; PS00450; ACONITASE_1; 1.
CC PROSITE; PS01244; ACONITASE_2; 1.
CC Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.
CC METAL 360 360 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
CC METAL 421 421 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
CC METAL 424 424 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
CC CONFLICT 291 291 N -> TLKH (IN REF. 1).
CC CONFLICT 423 423 I -> M (IN REF. 1).
CC CONFLICT 459 459 M -> I (IN REF. 1).
CC CONFLICT 744 744 R -> K (IN REF. 1 AND 4).
CC SEQUENCE 779 AA; 85794 MW; BD409A9702AE3E57 CRC64;

Query Match 60.6%; Score 2456.5; DB 1; Length 779;
Best Local Similarity 63.1%; Pred. No. 2.6e-158;
Matches 486; Conservative 93; Mismatches 152; Indels 39; Gaps 10;

Qy 8 PQTLYDKVLOAHVVDKLDGTWLLYIDRHLVHEVTSPOAFEGLEGRNAGRVKRRPDCITLATT 67
Db 9 PRTLYDKVFDHVHVDENGSGFLYIDRHLVHEVTSPOAFEGLEGRNAGRVKRRVDCITLTV 68
Qy 68 DHNVPTTSRKALKDIASPIKEDDSRTQCVTLLENVKEFGVTYFGLSDKRGQIVHVGPEQ 127
Db 69 DHNPTESRKNFKSLDTPIKQTSRLQVKTLENNVKGVPYFGVSGDARQGIIVHTIGPEE 128
Qy 128 GFTLPGTWVCGDSHTSTHGAFALAFGICTSEVHVLTATQCLITKRSKNMRIQVGDGELA 187
Db 129 GFTLPGTWVCGDSHTSTHGAFSLAFGIGTSEVHVLTATQTIQAKSKNMRITVNGKLS 188
Qy 188 PGVSSKDVVLHAIGIIGTAGGTGAVTEFCGVSIRLSMEARMSICNMTSEGGARAGQWAP 247
Db 189 PGITSKOLILYIIGLITAGGTGCVIEFAGEAIEALSMEARMSMCNMAIEAGRAGMKIP 248
```


QY 248 DEITFEYLKGRPLAPKXDSPEWHKATQYWKLOSPGAKYDIDVDITDAKDVIPTLTWGT 307
Db 249 DEITFEYLKGRPLAPK--GAEMEKAVAWYKTLKTDEGAKFHEINEIAVDVPIPTTWGT 306
QY 308 PEDVVPITGVDPDETEATEAKKADGRMLQYMGKAGTPEMDIVVDKVFISGCTNSRIE 367
Db 307 PQDALPITGVSVPDPKAVTDPFKSGMEBALAVMGLEPMTPLKSTVNDKVFISGCTNSRIE 366
QY 368 DLRAAAAVVKGKKAIPNVKSAVVVPGSLVYTOAEIEGLDKIFEEAGFEWRBAGCSMCLG 427
Db 367 DLRAAAAVVGGOKLASINIKLAMVVGSLVYKQAEGLDKIFQAGFEWRBAGCSICLG 426
QY 428 MNPDIILAPQERCASTSNRNFEGROGAGRTILMSPVMAAAGIVKGLADVRLTYK--- 484
Db 427 MNPDIILAYERCASSTNRNFEGRQALSRTHLMSPVMAAAGIAGFPVDIRBF-EYKQD 485
QY 485 -ASPHI-----AAQYKSTVTKPHYDERINQDAHEKDITADI PEDNNGHTNYS 531
Db 486 QSSBKVEVTSDEKELESAAVDHAEVPVQ---EDAPQDI-ANDELKDI PVKSDDIIPAKFS 541
QY 532 ASVGTSAGLPKFTLLKGIAPLEKAVNDTDALIPKQPLKTIKRTGLAGNALFEYEMRNEDG 591
Db 542 -----SSGKMPFLTLEGISAPLDKANVDTDAIIPKQPLKTIKRTGLKGLFEYEMFRKXD 596
QY 592 ----TEKSDPVLNKEPYKASILVCTGANFGCGSSREHAPMALNDFGINSVIAPSADIFF 648
Db 597 QGRDOEDPVLNVEPMEAEILVVTGDNFGCGSSREHAPMALNDFGINSVIAPSADIF 656
QY 649 NSPFGKMLPPIPIDOQOIEAIAEABAGKEIVDLPNOLIKNATGETICT- FEYEEBPK 707
Db 657 NSPFGKMLPPIPIDOQOIIIDKLIPIANKGSKLVDLPNOKLIDSGNVLVDHFEIEBPK 716
QY 708 HCLVNGLDIDIGLTQMOMEDKIAEFAKMTRETPWLDGTGYL-----XRX 750
Db 717 HCLVNGLDIDIGITLQKEEYISRVEALREKXSFLEGGSKLLKFDNVPRKX 766
RESULT 7
ID LEU2_CANMA STANDARD; PRT; 770 AA.
AC 000464;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-isopropylmalate dehydratase (EC 4.2.1.33) (Isopropylmalate
isomerase) (Alpha-IPM isomerase) (IPMI).
GN LEU.
OS Candida maltosa (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxId=5479;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=14;
RA Becher D., Jomantienne R., Schulze S., Bode R., Oliver S.G.;
RU Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
and 3-isopropylmalate, via the formation of 2-isopropylmalate.
CC - CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +
H(2)O.
CC - CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
isopropylmalate.
CC - PATHWAY: Leucine biosynthesis; second step.
CC - SUBUNIT: Monomer (By similarity).
CC - SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
CC -----
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CC -----
DR EMBL; U60167; AAB0335.1; -.
DR InterPro; IPR000573; Aconitase_C.
DR InterPro; IPR001030; Aconitase_N.
DR InterPro; IPR004430; Leuc.
DR InterPro; IPR004431; Leud.
DR Pfam; PF00330; aconitase; 1.
DR Pfam; PF00694; aconitase; 1.
DR PRINTS; PR00415; ACONITASE.
DR ProDom; PD000511; Aconitase_N; 1.
DR TIGRFAMs; TIGR00170; leuc; 1.
DR TIGRFAMs; TIGR00171; leud; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
KW Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.
FT METAL 354 354
FT METAL 415 415 (BY SIMILARITY).
FT METAL 418 418 (BY SIMILARITY).
SQ SEQUENCE 770 AA; 85317 MW; CBIC26A56D7C3C1A CRC64;
Query Match 59.6%; Score 2417.5; DB 1; Length 770;
Best Local Similarity 61.9%; Pred. No. 1.1e-155;
Matches 491; Conservative 79; Mismatches 178; Indels 45; Gaps 12;
QY 7 TPQTLVYDKVLQAHVDEKLDGTVLYIYDRHLVHEVTSPOAFEGILRNAGKRVPRDCTLAT 66
Db 2 SPKTLVDKFEEDHIVVEDESGSNLLYIDRHLVHEVTSPOAFEGILRNAGRTVRRDCTLAT 61
QY 67 TQHNVTTSRKMLKDIASFKEDEDSRTQCTLEENYVEFGVYFGSLDKOGIVHVGPE 126
Db 62 VQNNLPTIRVNEKTLTFTFDQDSRLQVOTLEQNVNDFPVYTFGMVDDQGIYHVGPE 121
QY 127 QGFTLLPQTVVCGSDSTSTHGAFALAFGIGTSEVEHVLATQCLITRKSMMRIQVNGEL 186
Db 122 QGFTLLPQTVVCGSDSTSTHGAFALAFGIGTSEVEHVLATQCLITRKSMMRIQVNGEL 181
QY 187 APGVSSKDVVLAHGIITGAGTGAIVIEFCGSVIRISLMEARMSICMNSIEGARGAVYA 246
Db 182 SEGITSKDVLVHIGVIGTAGTGCVIEFAGKAIEDLSMEARMSICMNAIEAGARGAVIK 241
QY 247 PEITFEYLKGRPLAPKXDSPEWHKATQYWKLOSPDGAKYDIDVDITDAKDVIPTLTWGT 306
Db 242 PEITFEYLKGRPLAPKGD--EWEKALKYKTLHTDAGALHYDIKLAASIVPTLTWGN 299
QY 307 SPEDVVPITGVDPDETEATEAKKADGRMLQYMGKAGTPEMDIVVDKVFISGCTNSRI 366
Db 300 SPQDALPITASVDPDPANVSPPIKSGMERALKYQGLTPNTPFVYIKHKAFIGSCTNSRI 359
QY 367 EDIRAAAVVKGKKAIPNVKSAVVVPGSLVYTOAEIEGLDKIFEEAGFEWRBAGCSMCL 426
Db 360 EDIRAAAVKAKGHKADNVYLVVPGSLIKQAEKEGDKIFESAGFTWRBAGCSMCL 419
QY 427 GNPDIILAPQERCASTSNRNFEGROGAGRTILMSPVMAAAGIVKGLADVRLTYKAS 486
Db 420 GNPDIILDEERCASSTNRNFEGRQARSRTILMSPVMAAAGIAGFPVDIRBF-EYKQD 478
QY 487 PHIAQYKSTVTKPH-VDERINQDA--HEKDITADI PEDNNGHTNYSASVGSAGLPK 542
Db 479 -----DEPSITIEHEVEDKELODAYIEHEKEIIEGPR-GTEARSTTSLKMNQNSKKPN 531
QY 543 FTLK-----GIAAPLEKAVNDTDALIPKQPLKTIKRTGLAGNALFEYEMRNEDG 591
Db 532 QMLIKVNPITVLPFLGITAIPVYKAVNDTDALIPKQPLKTIKRTGLKNGFEYESRFVYMP 591
QY 592 TEK--SDPVLNKEPYKASILVCTGANFGCGSSREHAPMALNDFGINSVIAPSADIFFN 649
Db 592 MYRCQDHPVLNVEPYQOABLIVTGNFNGCGSSREHAPMALNDFGINSVIAPSADIFYN 651
QY 650 NSPFGKMLPPIPIDOQOIEAIAEABAGKEIVDLPNOLIKNATGET----ICFEEVEEF 705
Db 652 NSPFGKMLPPIPIDOVIVESKLVVVGKHKLTIDLPNQQIKD--GEFGDVLIEKFDVEEF 709
QY 706 RKHCLVNGLDIDIGLTQMOMEDKIAEFAKMTRETPWLDGTGYLARKKGGKLAAYAVPPT 765

Query Match 51.2%; Score 2076; DB 1; Length 644;
Best Local Similarity 68.8%; Pred. No. 9.9e-133;
Matches 407; Conservative 60; Mismatches 111; Indels 14; Gaps 6;


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CC -1- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +
CC H(2)O.
CC -1- CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
CC isopropylmalate.
CC -1- PATHWAY: Leucine biosynthesis; second step.
CC -1- SUBUNIT: Heterodimer of leuc and leud (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ591793; CAC47785.1; -.
CC EMBL; AJ296268; CAC14578.1; -.
CC InterPro: IPR001030; Aconitase_N.
CC InterPro: IPR004430; Leuc.
CC Pfam: PF00330; aconitase; 1.
CC ProDom: PD000511; Aconitase_N; 1.
CC TIGRfam: TIGR00170; leuc; 1.
CC PROSITE; PS00450; ACONITASE_1; 1.
CC PROSITE; PS01244; ACONITASE_2; 1.
CC Leucine biosynthesis; lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
KW METAL 350 350 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 410 410 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 413 413 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT CONFLICT 31 31 R -> C (IN REF. 2).
FT CONFLICT 96 96 F -> L (IN REF. 2).
FT CONFLICT 270 270 T -> M (IN REF. 2).
FT CONFLICT 371 371 A -> S (IN REF. 2).
SQ SEQUENCE 469 AA; 50994 MW; 22A2F7D040645726 CRC64;

Query Match 40.3%; Score 1636; DB 1; Length 469;
Best Local Similarity 66.0%; Pred. No. 3,4e-103;
Matches 313; Conservative 57; Mismatches 96; Indels 8; Gaps 3;

OY 6 STPQTLVKVIAQAVHVDKLDGTVLLYIDRLHVEHVSPOAFEGIRNAGRVRPDCILA 65
DB 2 SAPRTLYDKIWDHVDVQDDGTCILYIDRLHVEHVSPOAFEGIRNAGRVRPDCILA 61
OY 66 TTDHNVPTTSKALKDIASTFKEDDSRTQCVTLLENVKEFGTVFGSLDKRQGIHVHVG 125
DB 62 VVDHNVPTSPDRHGG-----TKNEESRIQVEBALARNADPGEVEYSEMDKRGIVHVG 116
OY 126 EOGFTLPCTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVALTOCLITRKSRKMRIOVDGE 185
DB 117 EOGFTLPCTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVALTOCLITRKSRKMRIOVDGE 176
OY 186 LAPGVSSKDVVLAHIGIIGTAGTGAVIEFCGSVIRLSMEARNSICMSIEGGRAGMV 245
DB 177 LPPGVTAADIIILAIIGETAGTGTHVIEFAGEAIRLSMEGRMTVCMMTIEGGRAGLI 236
OY 246 APDDITTEYLKGRPLAPKXVSPPEWHKAKOVKKNOSDPGAKYDIDVDFADADIVTLLNG 305
DB 237 APDDITTEYLKGRPLAPKXVSPPEWHKAKOVKKNOSDPGAKYDIDVDFADADIVTLLNG 294
OY 306 TSPEDVVPITGVDPETFAATEAKKADGRMLQYVGLKAGTIPMEDIPYDKVFIGSCINSR 365
DB 295 SSPEDVVSQGVVNPDDIOBETKRTSKMRALDWGLKPGTKITDIALIDRVFIGSCINR 354
OY 366 IEDIRAAAVVVKRKAQNVKSAVVPSSGLVKTQAESEGLDKITEEAGFEKREAGCSNC 425
DB 355 IEDIRAAVVEVVEGRKVAFTV-SAMIVPSSGLVKEQAEAGDKITEKKEGFDWREPGCSNC 413
OY 426 LGMPDILAPORCASTNRNPEGQAGGRTTHLMSPVMAAAGIVGLADVRK 479
DB 414 LAMPDRLLKPGRCASISNRNPEGQGRKTHLSPVMAAALAAVAAGFVDIR 467

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RESULT 10
LEU2_BRUME STANDARD; PRT; 469 AA.
ID LEU2_BRUME
AC 08YJC9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE (isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMT).
GN LEUC OR BMEI0157.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
ON NCBI_TaxID=29459;
RX STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA Delvecchio V.G., Kapral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyriides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -1- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC and 3-isopropylmalate, via the formation of 2-isopropylmalate.
CC -1- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +
CC H(2)O.
CC -1- CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
CC isopropylmalate.
CC -1- PATHWAY: Leucine biosynthesis; second step.
CC -1- SUBUNIT: Heterodimer of leuc and leud (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC SUBFAMILY.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE009458; AL51339.1; -.
CC InterPro: IPR001030; Aconitase_N.
CC InterPro: IPR004430; Leuc.
CC Pfam: PF00330; aconitase; 1.
CC PRINTS; PR00415; ACONITASE.
CC ProDom: PD000511; Aconitase_N; 1.
CC TIGRfam: TIGR00170; leuc; 1.
CC PROSITE; PS00450; ACONITASE_1; 1.
CC PROSITE; PS01244; ACONITASE_2; 1.
CC Leucine biosynthesis; lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
KW METAL 350 350 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 410 410 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 413 413 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 469 AA; 50692 MW; 14442D949C40BCF CRC64;

Query Match 39.7%; Score 1611; DB 1; Length 469;
Best Local Similarity 66.8%; Pred. No. 1,6e-101;
Matches 316; Conservative 51; Mismatches 98; Indels 8; Gaps 3;

OY 6 STPQTLVKVIAQAVHVDKLDGTVLLYIDRLHVEHVSPOAFEGIRNAGRVRPDCILA 65
DB 2 SAPRTLYDKIWDHVDVQDDGTCILYIDRLHVEHVSPOAFEGIRNAGRVRPDCILA 61
OY 66 TTDHNVPTTSKALKDIASTFKEDDSRTQCVTLLENVKEFGTVFGSLDKRQGIHVHVG 125
DB 62 VVDHNVPTSPDRHGG-----PDRINGONESRIQVEBALARNADPGEVEYSEMDKRGIVHVG 116
OY 126 EOGFTLPCTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVALTOCLITRKSRKMRIOVDGE 185

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Db 117 EQGFTLPGMTIVCGDSHTSTHGAFALAHGIGTSEVHLVATQTLQKAKNMLVRVDGK 176
Qy 186 LAPGVSSKVVHLHAIGIITAGGTGAVIEFCGVSIRLSMEARMSICNMSIEGGARAGMV 245
Db 177 LPAGVTAQDIVLAIIGIITAGGTGAVIEYAGEAIRLSMEGRWICNMSIEGGARAGLI 236
Qy 246 APDEITFEYLKGRPLAPKYDSPWHKATQYWKNLQSDPGAKYDIDVFDIAKDVIPTLTWG 305
Db 237 APDEITFEYIKGRPAPQGETLE--QAINYWKTLHSDGAEHFDKIVTLTDAGSLPPIVSWG 294
Qy 306 TSPEDVVPITGVVDPPTFTFAEAKADGRMLQYMGKAGTGMEDIPVDKVFISCTNSR 365
Db 295 SSPEDVSVTVGVNPDIDIAETKRASKRWALDYMGKPGTKITDIAVDRVFIGSCTNGR 354
Qy 366 IEDLRAAAAVVGRKAPNVKSAWVPGSLVKVTKQAEIEEGDKIFEEAGFEWREAGCSMC 425
Db 355 IEDLRAAAKVVEGKVAPT-V-NAMIVPGSLVKVKEQAEGLHKIFIEAGFDWRPFGCSMC 413
Qy 426 LGMNPDIAPQERCASTSNRNFEGQAGGRTHLMSVPMAAAAGIVGKLVDR 478
Db 414 LAMNDRLLKPGERCASSTNRNFEGQGFGRTHLVSPAMAAAAGIAGHFVDIR 466

RESULT 11
LEU2_AGRTS
ID LEU2_AGRTS STANDARD; PRT; 469 AA.
AC Q8UB9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE (isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN LEUC OR ATU2709 OR AGR C.4910.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quorlo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
CC -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC and 3-isopropylmalate, via the formation of 2-isopropylmaleate +
CC -!- CATALYTIC ACTIVITY: 3-isopropylmaleate = 2-isopropylmaleate +
CC H(2)O.
CC -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC isopropylmalate.
CC -!- PATHWAY: Leucine biosynthesis; second step.

```

```

CC -!- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
CC -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC SUBFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AE009217; AAL43690.1; -.
CC EMIL; AE008184; AAK8428.1; ALT INIT.
CC InterPro; IPR001030; Aconitase_N.
CC InterPro; IPR004430; LeuC.
CC Pfam; PF00330; aconitase; 1.
CC PRODOM; PD00511; Aconitase_N; 1.
CC TIGRFAMs; TIGR00170; leuC; 1.
CC PROSITE; PS00450; ACONITASE 1; 1.
CC PROSITE; PS01244; ACONITASE 2; 1.
CC Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
KW METAL 350 350 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 410 410 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 413 413 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 469 AA; 51048 MW; F8EFFE03DA610D39 CRC64;

Query Match 39.1%; Score 1584; DB 1; Length 469;
Best Local Similarity 65.4%; Pred. No. 1.le-99;
Matches 310; Conservative 52; Mismatches 104; Indels 8; Gaps 3;

Qy 6 STPQTLYDKVLQAHVDEKLDTGLLYIDRHLVHEVTSQAEGLRNAGKVRPRDCTLA 65
Db 2 SAPRTLXDKIWDHVVNRDPDGTCLLYIDRHLVHEVTSQAEGLRIAGRPVHSPRTLA 61
Qy 66 TTDHNVPTTSKALKDIASFIEDDSRTQCVLEENVEFGVYFGLSKRQGIHVHVG 125
Db 62 VVDHNVPTTA-----DRLEGINKESRIQVEALAQNAKEFGVEYYSERDKRQGIHVHVG 116
Qy 126 EQGFTLPGTIVVCGDSHTSTHGAFALAHGIGTSEVHLVATQCLITKSKNMRIOVDGE 185
Db 117 EQGFTLPGMTIVCGDSHTSTHGAFALAHGIGTSEVHLVATQTLQKAKNMLVRVDGK 176
Qy 186 LAPGVSSKVVHLHAIGIITAGGTGAVIEFCGVSIRLSMEARMSICNMSIEGGARAGMV 245
Db 177 LPESVTAQDIVLAIIGIITAGGTGAVIEYAGEAIRLSMEGRWICNMSIEGGARAGLI 236
Qy 246 APDEITFEYLKGRPLAPKYDSPWHKATQYWKNLQSDPGAKYDIDVFDIAKDVIPTLTWG 305
Db 237 APDEITFDYIKGRPAPKGETLE--QAIAYWKTLKSDGAEHFDKIVVILDAANLPPVSWG 294
Qy 306 TSPEDVVPITGVVDPPTFTFAEAKADGRMLQYMGKAGTGMEDIPVDKVFISCTNSR 365
Db 295 SSPEDVSVTVGVNPDIDIEENKRTSKRWALDYMGKPGTKITDIAVDRVFIGSCTNGR 354
Qy 366 IEDLRAAAAVVGRKAPNVKSAWVPGSLVKVTKQAEIEEGDKIFEEAGFEWREAGCSMC 425
Db 355 IEDLRAAAKIVDGRKVASTV-SAMIVPGSLVKVKEQAEGLDKIFLDAGFEWREPGCSMC 413
Qy 426 LGMNPDIAPQERCASTSNRNFEGQAGGRTHLMSVPMAAAAGIVGKLVDRK 479
Db 414 LAMNDRLLKPGERCASSTNRNFEGQGYKSRTHLVSPAMAAAAGIAGHFVDVRE 467

RESULT 12
LEU2_RHILO
ID LEU2_RHILO STANDARD; PRT; 469 AA.
AC Q98EF1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE (isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).

```

Db 237 AADTTTAAVYKDKRRAK--GAAMDALAAWTKLQSGEGAFKFDKVIULDAAKLPVTSWG 294

QY 306 TSPEDVVPITGVVDPDPETFAATEAKKADGRMLQYMGKAGTPEMEDIPVDKFFISCTNSR 365

Db 295 SSPEDVYVSGGVVNPPEEITDENKRTSKIRALDYMGTLPGTKRIDIALDRVFISCTNGR 354

QY 366 IEDRAAAAVYKGRKKA PNKYSAMVVGSGGVYKQAEEGIDKIPEEAGFPMREAGCSMC 425

Db 355 IEDRAAAKVTIEGKTVPRV-NAMIVPSSGLVKSQAEGSDKIFLAAGFPMREAGCSMC 413

QY 426 LGKMPDILAPQERCASTNSRNFEGROGAGRTHTMS PMAAAGIVGKLAADVRLKLTDXK 484

Db 414 LAAMDRLKPHKRCASISNRNFEGRGCKGKTHLVSPMAAAAALAGHFVIR--DWK 469

RESULT 13

LEUC CAUCR

ID LEUC CAUCR STANDARD; PRT; 479 AA.

AC Q9ABN0; 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)

DE (isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).

GN LEUC OR CC0196.

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;

OC Caulobacter.

OX NCBI_TaxId=155892;

OX [1]

RN SEQUENCE FROM N.A.

RP STRAIN=ATCC 19089 / CB15;

RC MEDLINE=21173698; PubMed=11259647;

RA Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

RA Pockock I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

RA Deboy R.T., Dodson R.U., Durkin A.S., Ginn M.L., Haft D.H.,

RA Kolony J.F., Smt J., Craven M.B., Khouri H., Shetty J., Berry K.,

RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

RA "Complete genome sequence of Caulobacter crescentus.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

RL

CC -1- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate

CC and 3-isopropylmalate, via the formation of 2-isopropylmalate.

CC

CC -1- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +

CC H(2)O.

CC

CC -1- CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-

CC isopropylmalate.

CC

CC -1- PATHWAY: Leucine biosynthesis; second step.

CC

CC -1- SUBUNIT: Heterodimer of Leuc and Leud (By similarity).

CC

CC -1- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1

CC SUBFAMILY.

CC

CC -----

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CC

CC

DR EMBL; AE005694; AAK2183.1; -

DR TIGR; CC0196; -

DR InterPro; IPR001030; Aconitase_N.

DR InterPro; IPR004430; Leuc.

DR Pfam; PF00330; aconitase; 1.

DR PRINTS; PR00415; ACONITASE.

DR PRODOM; PD000511; ACONITASE_N; 1.

DR TIGRFAMs; TIGR00170; leuc; 1.

DR PROSITE; PS00450; ACONITASE_1; 1.

DR PROSITE; PS01244; ACONITASE_2; 1.

KW leucine biosynthesis; lyase; iron-sulfur; 4Fe-4S; Complete proteome.

FT METAL 350 350 IRON-SULFUR (4FE-4S) (BY SIMILARITY).

```

CC -I- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC isopropylmalate.
CC -I- PATHWAY: Leucine biosynthesis; second step.
CC -I- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
CC -I- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE002454; AAF41435.1; -.
DR TIGR; NMB1036; -.
DR InterPro; IPR001030; Aconitase_N.
DR InterPro; IPR004430; LeuC.
DR Pfam; PF00330; aconitase; 1.
DR PRINTS; PR00415; ACONITASE.
DR ProDom; PD000511; Aconitase_N; 1.
DR TIGRFAMS; TIGR00170; leuc; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
DR Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
KW METAL 349 349 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 410 410 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 413 413 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 469 AA; 50843 MW; D538C334E590E4E0 CRC64;
Query Match 38.2%; Score 1548.5; DB 1; Length 469;
Best Local Similarity 63.6%; Pred. No. 2.7e-97;
Matches 302; Conservative 62; Mismatches 102; Indels 9; Gaps 3;
QY 7 TPQTLYDKVLQAHVDEKLDGTLLYIDRLHVHEVTSPOAFEGRLNAGRKVRPRDCTLAT 66
DB 2 TAQTLYDKLWNHVVREEDGTLLYIDRLHVHEVTSPOAFEGRLKVGAKRLWRIDSVVST 61
QY 67 TDHNPVTSKALKDITASFKEDDSRTQCVTLEENKVEFG-VTFYGLSDKRGQIVHVGP 125
DB 62 ADHNTPT-----GDWDKGIQDPISKQLQVDLTLDKNIKEFGALAYFFPFMDKGQGIHVHMG 115
QY 126 EQGFTLPGTVCGDSHTSTHGAFGALAFGIGTSEVHEVLATOCILTKRSKNMRIQVDGE 185
DB 116 EQGATLPGMTVCGDSHTSTHGAFGALAHGIGTSEVHTMATOCITAKSKSLDISVDGK 175
QY 186 LAFGVSSKQYVLHAIGIIGTAGTGAVIEFGSVIRSLSMEARMSICNMSIEGGARAGMV 245
DB 176 LKAGVTAQDVALYIIQIGTAGTGVAIEFGGEAIRLSWSERMLCNMAIEAGRSGMV 235
QY 246 APDEITPEYLKGRPLAPKYSPEWHKATQVKNVQLQSDPGAKYDIDVPIDAKOIVPTLTWG 305
DB 236 AVDQTTIDYVKDFPFAPEGEA--WDKAVEYWRTLVSDGAVDFKDYRFNAEDIEPQVTWG 293
QY 306 TSPEDVVPITGVVPDDETPATEAKKADGRMLQYMGKAGTGMEDIPVDKVFVIGSCTNSR 365
DB 294 TSPEWMLDSSKVPNPAETDTPVKRSGMERALYMGLEAGTPLNEIIPVDIVFVIGSCTNSR 353
QY 366 IEDLRAAAAVKGRKKAPNVKSMVVPVSGSLVKTQAEELGDKIFEEAGFEWEAGCSMC 425
DB 354 IEDLREAAAIADKRAANQVRLIVPGSGLVKEQAEKGLDKLFI EAGFEWEPEGCSMC 413
QY 426 LGNPDILAPQERCASTSNRNFEGRQAGRTHLMSFVMAAAAGIVGKLADVRKL 480
DB 414 LAMNADRLTPGORCASTSNRNFEGRQNGGRTHLVSPAMAAAAAATVGRFTDIRMM 468
RESULT 15
LEUC_NEIMA
ID LEUC_NEIMA STANDARD; PRT; 469 AA.
AC Q9JU82;
DT 15-JUN-2002 (Rel. 41) Created)

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DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE (isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN LEUC OR NMA1450.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae, Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holroyd S.,
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajadaram M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrett B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 22491."
RL Nature 404:502-506(2000).
CC -1- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC and 3-isopropylmalate, via the formation of 2-isopropylmalate.
CC -1- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +
CC H(2)O.
CC -1- CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
CC isopropylmalate.
CC -1- PATHWAY: Leucine biosynthesis; second step.
CC -1- SUBUNIT: Heterodimer of leuc and leud (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC SUBFAMILY.
-----
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-----
CC EMBL, AL162756; CAB84686.1; -.
DR InterPro; IPR001030; Aconitase_N.
DR InterPro; IPR004430; Leuc.
DR Pfam; PF00330; aconitase; 1.
DR PRINTS; PR000415; ACONITASE.
DR PRODOM; PD000511; Aconitase_N; 1.
DR TIGRfam; TIGR00170; leuc_1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
KM Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT METAL 349 349 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 410 410 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 413 413 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 469 AA; 50783 MW; 89AE349827DA25DB CRC64;
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Query Match 38.1%; Score 1545.5; DB 1; Length 469;
Best Local Similarity 63.4%; Pred. No. 4.4e-97;
Matches 301; Conservative 62; Mismatches 103; Indels 9; Gaps 3;

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Db 176 LKAGYAKDVALYIIIGIGTAGCTGYAIEFGGEAIRSLMEGRMTLCNMAIEAGRSGMV 225
Qy 246 APPETIPEYLKGRPLAKRYDSPENHAKTOYWKLOQSPGAKYDIDVFIDAKDVPILTWG 305
Db 236 AVDDQTTIDYVKDKRFAEBEGBA--WDKAVEYWRTLVSDGAVFQDEYFRFNAEDIEPQYTW 293
Qy 306 TSPEDVPIFGVVPDEPTFATLTKAKADGRMLQYMGKAGPMEDIVDVKYFGSCNRSR 365
Db 294 TSPDMVLDISSKVPNPAEETDPVRSGMERALEYWGIEAGTPILEIVDVIFIGSCNRSR 353
Qy 366 IEDRAAAAVVKGKAPNYKSAMVVPVSGLVKTOAEEDGDKIFEEBAGFEMREAGSCMC 425
Db 354 VEDUREAAALAKKORRKAANYRVILVPGSGLVGEQAKKEGDKIFLAGFEMRERPGSCMC 413
Qy 426 LGMNPDLIAPOERCASNTSNRFEGRGAGGRTHTLMSFVMAAAGIVGLADVRKL 480
Db 414 LANMADRLTRQRCASTSNRNFEGRGNGRTHLVSPAMAAAVATGRFTDIRMK 468

RESULT 16
LEUD_XANCP STANDARD; PRT; 479 AA.
ID LEUD_XANCP
AC P58949;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE (isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN LEUC OR XCC331.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ANCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Rehnach F.C., Farah C.S., Furian L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., de Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Canavan F., Cardoso J., Chambergo F., Ciapina L.P.,
RA Ciarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria U.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sema U.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
CC -1- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC and 3-isopropylmalate, via the formation of 2-isopropylmalate.
CC -1- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +
CC H(2)O.
CC -1- CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
CC isopropylmalate.
CC -1- PATHWAY: Leucine biosynthesis; second step.
CC -1- SUBUNIT: Heterodimer of leuc and leud (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC SUBFAMILY.
-----
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CC or send an email to license@isb-sib.ch).

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D5	181	PFGVYAKDI VLVAV LGKLTJAGGNGHAFAGSAI RALSMGRWTI CNNSI EAGARVGWVA	243
Qy	247	PDEITFYLKGRPLAPKYDSPWHKATQYWKNIQSDPGAKYDIDVFIDAKDVIPTLTWCT	306
Db	241	VDEKTIYVYKGRFPAPK-CADWDAVALWRTLVSDADASFDTVVEIRAEKTPQVSWT	298
Qy	307	SPEDVPIPGVDPDPETAFATEAKKADGRRLQIYWGKLKAGCTPMEDI PVDKVFYIGSCTNSRI	366
Db	299	SPENWVAIDQOVPDPAAEQDPTKXDSIFORALKYIYWGRLRANQPTIEIHLDRVFIIGSCTNSRI	358
Qy	367	EDLRAAAAVYVGRKAPNVKSAMVPGSGIYLVKTOABEEGLDKIFEBAGFEWREPAGCSMCL	426
Db	359	EDLRAAAAVAKGRKVASTIKQALVPGVSGIYVKAQAEGLDKIFLDAGFEWREPAGCSMCL	418
Qy	427	GMNPDIIAPQERCASCTNSRNPFGQAGGRTHLMSPVMAAAAGIVGKLADVRKL	480
Db	419	AMNPKLGSGEHCASCTNSRNPFGQAGGRTHIVSPAMAAAAAVSGHFVDVREL	472

CC	ENML; AE011993; AAM38301.1; --				
DR	PROSITE; PS00450; ACONITASE_1; 1.				
DR	PROSITE; PS01244; ACONITASE_2; 1.				
DR	Lecuticne biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.				
KW	METAL 353 353 IRON-SULFUR (4FE-4S) (BY SIMILARITY).				
FT	METAL 414 414 IRON-SULFUR (4FE-4S) (BY SIMILARITY).				
FT	METAL 417 417 IRON-SULFUR (4FE-4S) (BY SIMILARITY).				
SQ	SEQUENCE 479 AA; 51506 MW; 70111DB3123FB0A6 CRC64;				
	Query Match 37.3%; Score 1514.5; DB 1; Length 479;				
	Best Local Similarity 63.5%; Pred. No. 5.6e-95;				
	Matches 301; Conservative 51; Mismatches 119; Indels 3; Gaps				
QY	7 TPQTLDVKVLQAHVDEKLDGTVLLIYDRLHVEHTVSPOAFGLRNAGRKVRPDCDTLAT 66	:	:	:	:
Dd	1 : : : : : : : : : : : : : :	:	:	:	:
Dd	2 TARTLDKWLHEHVTRRDGSLIYIDRHILHEVTSPQAFGLRAGRKPRRIDANIAT 61	:	:	:	:
QY	67 TDHNVPPTGRKALKDIASPIKEKDDSTQCVTLEENVKEFGVTYFGLSDKRQGVIVHVGPGE 126	:	:	:	:
Dd	62 PDHNPPTTAAERGGLES-ISDEVSRLOVQTTLDNCCDFGLEFKMDARQGIHVHVGPGE 120	:	:	:	:
QY	127 QGTTLPGTTCVCGDSHTSHGAFALAPGIGTSSEVHHVLATOCGLTKRSKNMRIQVDGBL 186	:	:	:	:
Dd	121 QGATLPGMTVCVCGDSHTSHGAFALAHAGIGTSSEVHHVLATCLIAKKNNMQVRVEGLT 180	:	:	:	:
QY	187 APGVSKDVVLAHIGAIGTAGGTGAVIEFCGSVIRLSMEARMSICNMSEGGARAGMVA 246	:	:	:	:
Dd	181 PFGVTAKDIVLAVIGIKGTAGGNHGALEFAGSAIRTLSMEGRTMCNMAIEAGARVGWA 240	:	:	:	:
QY	247 PDEITEYLKGRPLAKPYDSEPWHKATQWKMLQSDPGAKYDIDVFIDAKDIVPTLTWGCT 306	:	:	:	:
Dd	241 VDEKTAYVRGFPAFK--GAHWDAVALWSLTVSDPDHFVTVELRAEDIKPQVSWGT 298	:	:	:	:
QY	307 SPEDVVPIITGVVPDPPTFAATEAKADGRMLQVMGLKACTPMEDI PVDKVFI GSCINSRI 366	:	:	:	:
Dd	299 SPEWLVAIHQHPVDPPEAQEDPTKRDSIERALKYMGKANKOPTAIRLDRVFGSCTNSRI 358	:	:	:	:
QY	367 EDLRAAAANVKGKKAPNVKSAMVPGSGVIKTOABEEGLDKLFEEAGFEWEBAAGCSMCL 426	:	:	:	:
Dd	359 EDIRAAAAANVAKGRKVASTIKQALVPGSGVLVKAQAEEGLDKVFDADGFEWEBAAGCSMCL 418	:	:	:	:
QY	427 GMNPDLILAPQRCASNTSNRFEGRQAGGRTHLMSPVMAAAAGIVGLKADVRKL 480	:	:	:	:
Dd	419 ANMPDKLGSGEHCASNTSNRFEGRQAGGRTHLVSPAMAAAANSVGHFVDVREL 472	:	:	:	:


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RESULT 18
LEU2_PSEAE
ID LEU2_PSEAE STANDARD; PRT; 474 AA.
AC 09H2A3;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
DE LEUC OR PA3121.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Medman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reiter U., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RA opportunistic pathogen.";
RT Nature 406:959-964(2000).
RL
CC -1- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC and 3-isopropylmalate, via the formation of 2-isopropylmalate.
CC -1- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +
CC H(2)O.
CC -1- CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
CC isopropylmalate.
CC -1- PATHWAY: leucine biosynthesis; second step.
CC -1- SUBUNIT: Heterodimer of leuc and leud (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC SUBFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AE004736; MAG06509.1; -
DR InterPro; IPR001030; Aconitase_N.
DR Pfam; PF00330; aconitase_1.
DR PRINTS; PR00415; ACONITASE.
DR PRODOM; PD000511; Aconitase_N; 1.
DR TIGRFAHS; TIGR00170; leuc1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
DR Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT METTL 353 353 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METTL 414 414 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METTL 417 417 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 474 AA; 51042 MW; 7B4A0F500C28BC CRC64;
Query Match 37.2%; Score 1507.5; DB 1; Length 474;
Best Local Similarity 62.5%; Pred. No. 1.6e-94;
Matches 295; Conservative 61; Mismatches 113; Indels 3; Gaps 2;
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Db 64 HNVPTTRERKGGIAA-IADERSRLQVQTLIDENCDDFGITEFKKNDVRQIVHVVGPEQG 122
QY 129 FTLPPTTVCSDSHSTHGAFGALAFGIGTSEVEHVLTATOCITTKSKNNRIQVDELAP 188
Db 123 ATLPPTTVCSDSHSTHGAFGALAFGIGTSEVEHVLTATOCITTKSKNNRIQVDELAP 182
QY 189 GVSSKDVVLHAIGITGAGTGAVIEFGSSVIRSLSEAMMSICNMSIEGARGAWAPD 248
Db 183 GTAKDVIYAVIGRITAGANGHAIIFAGSAIRDLSTIEGRTICNMSIEAGARVGLVAVD 242
QY 249 EITFEYLRKPLAPKDPSEMHKATQYWKLOSDPPAKYIDVFIIDAKDVIPTLTMTKSTP 308
Db 243 QKTIDVKKRPFPAP--SAQWDQVAACWQGLVSDADAFDTVLVEDLAQYIKPYQVSWGTSP 300
QY 309 EDVVPITGVPPPEPTPATPAKAKADGRMLQYMGAKAGTPMEDIPVDKVFISGCTNSRIED 368
Db 301 EAVLVADQVPPPARSDPIKRSIERALKYMDLRPNQATTDIQLDRVFIISGCTNSRIED 360
QY 369 LRAAAAVVKGRKAPNVKAMVVPSSGLVKTQAEEGGLDKIFEAGFEWEDAGCSMCLGM 428
Db 361 LRAAAEVARGKVAATIKQALVPGSGLVKEQAEKEGLDRIFIEAGFEWEDAGCSMCLGM 420
QY 429 NPDILAPORCASTSNRNFEGRCAGGRTHMSPVMAAAGIYKGLADVRKL 480
Db 421 NPDRLSEGEHCSTSNRNFEGRCAGGRTHLVSPPMAAAAVNGRFIDREL 472
RESULT 19
LEU2_XYLFA
ID LEU2_XYLFA STANDARD; PRT; 474 AA.
AC 09PAX0;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
DE LEUC OR XF2375.
GN Xylella fastidiosa.
OS Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN=9asc;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Agencio M.,
RA Alverenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorcy H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Fetto J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garner W., Goldman S.G., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lampais M.R., Leite L.C.C.,
RA Lemos B.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Martino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miranda E.C., Miyaki C.Y., Monteiro-Vitollo C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhai A. Jr., Nobrega F.C., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Sanelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Salvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa";
RL Nature 406:151-159(2000).
```

CC -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC H(2)O.
CC -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC isopropylmaleate.
CC -!- PATHWAY: Leucine biosynthesis; second step.
CC -!- SUBUNIT: Heterodimer of leuc and leud (By similarity).
CC -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC SUBFAMILY.
CC
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CC
CC EMBL; AE004047; AAF85174.1; -.
CC InterPro; IPR001030; Aconitase_N.
CC Pfam; PF00330; aconitase; 1.
CC PRINTS; PR00415; ACONITASE.
CC PRODOM; PD000511; Aconitase_N; 1.
CC TIGRfams; TIGR00170; leuc; 1.
CC PROSITE; PS00450; ACONITASE_1; 1.
CC PROSITE; PS01244; ACONITASE_2; 1.
CC Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT METAL 353 353
FT METAL 414 414 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 417 417 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 474 AA; 51183 MW; 9985DF82B23750 CRC64;

Query Match 37.0%; Score 1498.5; DB 1; Length 474;
Best Local Similarity 63.1%; Pred. No. 6.7e-94;
Matches 298; Conservative 52; Mismatches 119; Indels 3; Gaps 2;

QY 9 QTLYDKVLQAHVDEKLDGTLLYIDRHLVHEVTSPOAFGLRNAGRKVRPDCATLTD 68
DB 4 KTLYSKLWDIHEVARDDGSSLLYIDRHLVHEVTSPOAFGLRNAGRKVRPDCATLTD 63

QY 69 HNVPTTSRKALKDASFKEDDSRTQCVTLLENVKEFGVTYFGLSKRGIVHVGPEQG 129
DB 64 HNVPTTKAERQGSLLS-IADTVSRSLQVTLDCNDDDFGFEFKMNDVRQGIHVHVGPEQG 122

QY 129 FTLPQTTVVCGDSHTSTHGAFGALAFGIGTSEVHVLAATCLITKRSKNMRIQVDGELAP 188
DB 123 ATLPQMTVVCGDSHTSTHGAFGALAHGIGTSEVHVLAATCLVTKRKNMQRVEGTLPLW 182

QY 189 GYSSKDWLHAIIGTAGTGAVIFPCGSVIRSLSMEARMSICNMSIEGAGRMVAPD 248
DB 183 GYTKADIVLALIGKIGTAGNGYAVFSGTIRALSNEGRMTICNMAIEAGARVMVAVD 242

QY 249 EITFEYKGRPLAPKYDSEPHKATQWKNLQSDPGAKYDIDVIDAKIVPTLTWTGSP 308
DB 243 EKTIIQYVHGRFPAPK--GSDWDAVAFWRGLVSDPDADFRVWVSELSAEIKPQVTWTGSP 300

QY 309 EDVVPITGVVDPDETATFAKADGRMLQYMGKAGTWMEDIPVDKVFIGSCNRSIED 368
DB 301 EMWSAVDQSVDPDERETDPVKESLIRALKYMGVLPQNDPITSIKLDRVFIGSCNRSIED 360

QY 369 LRAAAAVVKGKAPNVKSMVVPGLVKVTAEEGLDKIFEEAGFEWREAGSCMCLGM 428
DB 361 LRAAAEVVKGKRVASTVKQAMVVPGLVKAQAEVEGLDKIFEEAGFEWREPGCSMCLAM 420

QY 429 NPDILAPQRCASTNRNFEGRGACGRTMLSPVMAAAAGIVGKLADVRKL 480
DB 421 NPDKLGSGEHCASSTNRNFEGRGIGRTHLVSPMAAAAAAAGVGHFVDVREM 472

RESULT 20
LEU2_RALSO

ID LEU2_RALSO STANDARD; PRT; 469 AA.
AC Q8XX3;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE (isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
GN LEUC OR RSC1990 OR RS03558.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangelot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Gaspin C., Lavie M., Moisan A., Claudel-Renard C., Cumac S., Demange N.,
RA Siquier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
CC -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC -!- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmaleate +
CC H(2)O.
CC -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC isopropylmaleate.
CC -!- PATHWAY: Leucine biosynthesis; second step.
CC -!- SUBUNIT: Heterodimer of leuc and leud (By similarity).
CC -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch.)
CC
CC EMBL; AL646067; CAD15692.1; -.
CC InterPro; IPR001030; Aconitase_N.
CC InterPro; IPR004430; Leuc.
CC Pfam; PF00330; aconitase; 1.
CC PRINTS; PR00415; ACONITASE.
CC PRODOM; PD000511; Aconitase_N; 1.
CC TIGRfams; TIGR00170; leuc; 1.
CC PROSITE; PS00450; ACONITASE_1; 1.
CC PROSITE; PS01244; ACONITASE_2; 1.
CC Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
KW METAL 347 347 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 410 410 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 413 413 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 469 AA; 50796 MW; B451E964478AAE CRC64;

Query Match 36.8%; Score 1493; DB 1; Length 469;
Best Local Similarity 63.5%; Pred. No. 1.5e-93;
Matches 301; Conservative 53; Mismatches 110; Indels 10; Gaps 3;

QY 9 QTLYDKVLQAHVDEKLDGTLLYIDRHLVHEVTSPOAFGLRNAGRKVRPDCATLTD 68
DB 3 KTLYDKLWDDHVHTEEDGTTVLYIDRQLLHEVTSPOAFGLKLANRPVWRISANLAVSD 62

QY 69 HNVPTTSRKALKDASFKEDDSRTQCVTLLENVKEFGVTYFGLSKRGIVHVGPEQG 128
DB 63 HNVPTTDDR-----SHGADPVSQKLVQDTLDANCDSFGITQFMKTDKRGIVHVGPEQG 116

QY 129 FTLPQTTVVCGDSHTSTHGAFGALAFGIGTSEVHVLAATCLITKRSKNMRIQVDGELAP 188
DB 117 ATLPQMTVVCGDSHTSTHGAFGALAHGIGTSEVHVLAATCLLAKSKNMLKVEGTLPR 176

Oy	169	GVSSKDVVLLHAIIGITIGTGGTCGATVIEFCGSGYTRLSISMAKRSICMMS1EGGARAGAWAPD	24
Oy	168	GVSSKDVVLLHAIIGITIGTGGTCGATVIEFCGSGYTRLSISMAKRSICMMS1EGGARAGAWAPD	24
Db	177	GCTAADIVLAIIGKIGTGGTGGYMAEFGSARLALSMGRTIVCMMALEAGARAGMWVD	236
Oy	249	ETTFEYLGKRPAPPYKSDPEMHKATQYWKNLQSDPGATYDIDVFIDAKDIPVTLTWGTSR	308
Db	237	DTLLEYIKGRPPAPQ--GVMEQAVAYWRSLSHSDBGAFPDHVEIRAEIEIPQYSWGTSR	299
Oy	309	EDVPIITGVVPDPETFEATEAKKADGRMLQYWGELKAGTMEDIPDVKYFISGCTNSRIED	366
Db	295	EMWVSIEDRPDPDKEDKQPVKRNAMERALEVWALQPNVAIGDIRDKYFISGCTNSRIED	354
Oy	369	LRAAAAVVK--GRKAPVYKSMYVPGSGIVYKQAEFGGLDKIPEBAGFEFRERAGCSMCL	422
Db	355	MRAAAWVYOKLGGKRIASNVKLMVVPVGGSLVVEQAREGLKIFPAAGFEWREPGCSMCL	414
Oy	427	GNNPILAPQERCASTSNRNFEGRCAGGRTHTLMSPVMAAAAGIVGKLADVRL	480
Db	415	AMNADRLERGERCASTSNRNFEGRCAGGRTHTLMSPVMAAAALGHHVDVRL	468
RESULT 21			
LEU2_ECOLI	ID	LEU2_ECOLI	STANDARD; PRT; 465 AA.
AC	P30127	P30127	1-APR-1993 (Rel. 25, Created)
DT	01-NOV-1997	01-NOV-1997	(Rel. 35, Last sequence update)
DT	15-JUN-2002	15-JUN-2002	(Rel. 41, Last annotation update)
DE	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)		
DE	(isopropylmalate isomerase) (Alphaprm isomerase) (IPMI).		
GN	LEUC OR B0072		
OS	Escherichia coli.		
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		
CC	Escherichia.		
OX	NCBI_TaxID=562;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	MEDLINE=91088346; PubMed=2124684;		
RA	Rosenthal E.R., Calvo J.M.;		
RT	"Apidicolin inhibits DNA polymerase II of Escherichia coli, an		
RT	alpha-1ike DNA polymerase.";		
RL	Nucleic Acids Res. 18:7185-7186 (1990).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=K12;		
RC	MEDLINE=92234977; PubMed=1630901;		
RA	Isono T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,		
RA	Yura T., Mizobuchi K., Nakata A.;		
RT	"Systematic sequencing of the Escherichia coli genome: analysis of		
RT	the 0-2.4 min region.";		
RL	Nucleic Acids Res. 20:3505-3508 (1992).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=K12 / MG1655;		
RC	MEDLINE=97426617; PubMed=9278503;		
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,		
RA	Riley M., Davis D., Glasner J.D., Rode C.K., Mayhew G.F.,		
RA	Gregor J., Collado-VIDES, Kirpatrick H.A., Goeden M.A., Rose D.J.,		
RA	Mau B., Shao Y.;		
RT	"The complete genome sequence of Escherichia coli K-12.";		
RL	Science 277:1453-1474 (1997).		
RN	[4]		
RP	SEQUENCE OF 1-203 FROM N.A.		
RC	STRAIN=K12;		
RC	MEDLINE=94164169; PubMed=8119295;		
RA	Kirino H., Aoki M., Hayashi Y., Ohba M., Yamagishi A., Wakagi T.,		
RA	Oshima T.;		
RT	"Hydrophobic interaction at the subunit interface contributes to the		
RT	thermostability of 3-isopropylmalate dehydrogenase from an extreme		
RT	thermophile, Thermus thermophilus.";		
RL	Eur. J. Biochem. 220:275-281 (1994).		
RN	[5]		

[illegible]

```
Db 236 ETTFNKVGRLHAPK--GKPDFFDAVAVYKTLQTDGATFTDVTYVLOAEEISGQVWTGTP 293
QY 309 EDVVPITGVPPDPFTFATEAKKADRRMLQYMGKAGTPEMDIPVDKVFISGCTNSRIED 368
Db 294 GQVSVNDNIPDPASFADPVERASAEKALAYMGLKPGIPLTEVAIDKVFISGCTNSRIED 353
QY 369 LRAAAVVKGRKAPNVKSMVPGSGLVTKQAEAEGLDKIFEAAGFWRRAGGSMCLGM 428
Db 354 LRAAAEVVKGRKAPNVQVQ-ALVPGSGPVKAQAEAEGLDKIFIEAGFEWRLPGCSMCLAM 412
QY 429 NPDILAPQERCASTSNRNFEGRGQGRGTHLSPVMAAAAGIVGKLADVRKL 480
Db 413 NDRNLNPGERCASTSNRNFEGRGQGRGTHLSPVMAAAAVTGHFADIRMI 464

RESULT 22
LEU2_SALTY
ID LEU2_SALTY STANDARD; PRT; 465 AA.
AC F15717;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 3-isopropylmalate dehydratase large subunit 1 (EC 4.2.1.33)
DE [isopropylmalate isomerase 1] (Alpha-IPM isomerase 1) (IPMI 1).
GN LEUC1 OR LEUC OR STM0111.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]_TaxID=602;
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=90272436; PubMed=2190189;
RA Rosenthal E.R., Calvo J.M.;
RT "The nucleotide sequence of leuc from Salmonella typhimurium.";
RL Nucleic Acids Res. 18:3072-3072 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica setovar Typhimurium
RT LT2.";
RL Nature 413:852-856 (2001).
CC -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
CC -!- CATALYTIC ACTIVITY: 3-isopropylmaleate = 2-isopropylmaleate +
CC H(2)O.
CC -!- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)O = 2-
CC isopropylmaleate.
CC -!- PATHWAY: Leucine biosynthesis; second step.
CC -!- SUBUNIT: Heterodimer of leuc and leud (By similarity).
CC -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL; X51476; AAA35840.1; -
DR EMBL; M31047; AAA27155.1; -
DR EMBL; AE008699; AAL19075.1; -
DR PIR; S10171; S10171.
DR StyGene; SG10197; leuc1.
DR InterPro; IPR001030; Aconitase_N.
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DR InterPro; IPR004430; LeucC.
DR Pfam; PF00330; aconitase; 1.
DR TIGRFAMs; TIGR00170; leuc; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
KW Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
FT INIT_MET 0
FT METAL 346 346
FT METAL 406 406
FT METAL 409 409
FT CONFLICT 37 53
FT CONFLICT 345 345
FT CONFLICT 357 357
FT CONFLICT 361 364
FT CONFLICT 368 384
FT CONFLICT 410 412
SQ SEQUENCE 465 AA; 49654 MW; 014ED81AF5A19BB7 CRC64;

Query Match 36.4%; Score 1477.5; DB 1; Length 465;
Best Local Similarity 61.7%; Pred No. 1.7e-92;
Matches 291; Conservative 63; Mismatches 109; Indels 9; Gaps 4;

QY 9 QTLYDKVLQAHVVDKLDGTLLYIDRHVLVHEVTSQAFEGRLNAGRKVRRPDTLATTD 68
Db 2 KTLVEKLFDAHVVEAPNETPLLYIDRHVLVHEVTSQAFDGLRAHHRPVQPKTFATMD 61
QY 69 HNVPTTSRKALKDIASFKEDEDSRTQCVTLEENVEFGVYTYGLSKRQGIHVHIGPEQ 128
Db 62 HNVSTQT----KDINA--SGEMARIQMQLIKNCNEFGVELYDLNHPYQGIHVHMGPEQ 115
QY 129 FTLPGTTVCGDSHTSTHGAFCALAFGIGTSEVHVLAQTCLITKRSKNMRIQVDBGELAP 188
Db 116 VTLPGTTVCGDSHTATHGAFCALAFGIGTSEVHVLAQTCLITKQGRAKTWKIEVTGNAAP 175
QY 189 GVSSKDVVLHAIIGITAGTGAVIEFCGVSIRLSMEARMSICNMSIEGGARAGMVAPD 248
Db 176 GITAKDIVLAIIGTGSAGGTGHVVEFCGDAIRALSMEGRWMLCNMAIEWGAKAGLVAPD 235
QY 249 EITFEYLKGRPLAPKYDSEPHKATQYKNLQSDGAKYDIDVIDAKDIVPLTWTGTP 308
Db 236 ETTFNKVGRLHAPK--GRDFEAVEYWKTLTDDGATEDFTVVALRAEEIAPQVWTGTP 293
QY 309 EDVVPITGVPPDPFTFATEAKKADRRMLQYMGKAGTPEMDIPVDKVFISGCTNSRIED 368
Db 294 GQVSVNDNIPDPASFADPVERASAEKALAYMGLQPGVPLTDVAIDKVFISGCTNSRIED 353
QY 369 LRAAAVVKGRKAPNVKSMVPGSGLVTKQAEAEGLDKIFEAAGFEWRRAGGSMCLGM 428
Db 354 LRAAAEVVKGRKAPNVQVQ-ALVPGSGPVKAQAEAEGLDKIFIEAGFEWRLPGCSMCLAM 412
QY 429 NPDILAPQERCASTSNRNFEGRGQGRGTHLSPVMAAAAGIVGKLADVRKL 480
Db 413 NDRNLNPGERCASTSNRNFEGRGQGRGTHLSPVMAAAAVTGHFADIRSI 464

RESULT 23
LEU2_SALTY
ID LEU2_SALTY STANDARD; PRT; 465 AA.
AC Q82912;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE [isopropylmalate isomerase] (Alpha-IPM isomerase) (IPMI).
GN LEUC OR STY0130.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN-CT18;
RA MEDLINE=21534947; Pubmed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Comercon P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltruell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagers K.,
RA Krogh A., Larsen T.S., Leather A., Mien T.T., Holroyd S., Jagers K.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
CC -1- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC and 3-isopropylmalate, via the formation of 2-isopropylmalate.
CC -1- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +
CC H(2)O.
CC -1- CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
CC isopropylmalate.
CC -1- PATHWAY: Leucine biosynthesis; second step.
CC -1- SUBUNIT: Heterodimer of leuc and leud (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AL627265; CAD01268.1; -
CC InterPro: IPR001030; Aconitase_N.
CC Pfam: PF00415; ACONITASE.
CC PRINTS; PR00415; ACONITASE.
CC PRODOM; PD000511; Aconitase_N.1.
CC TIGRFAMs; TIGR00170; leuc.1.
CC PROSITE; PS00450; ACONITASE_1; 1.
CC PROSITE; PS01244; ACONITASE_2; 1.
CC KW Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
CC FT INIT MET 0
CC METAL 346 346 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
CC METAL 406 406 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
CC METAL 409 409 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
CC SEQUENCE 465 AA; 49684 MW; 4C23A8068C492DB CRC64;
CC -----
Query Match 36.4%; Score 1477.5; DB 1; Length 465;
Best Local Similarity 61.7%; Pred. No. 1,7e-92;
Matches 291; Conservative 63; Mismatches 109; Indels 9; Gaps 4;
9 QTVYDKVLQAVHVDKEDGTVLYLIDRLVHEVTSPOAFEGIRNARKVRPDCITLATTD 68
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
2 KTLVEKLFDAHVVEAENETPLYLIDRLVHEVTSPOAFDGRRAHHRVROGKFPATMD 61
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
69 HNVPTTSRKALKDIASFIKEDSDFTQCVLEENVEKFEVTVYFGLSDKQGIHVIVITEGG 128
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
62 HNVSTQF---KDIINA--SGEMARIQWELIKNCNEFGEVLEHLDNHPYQGIHVHVMGPEG 115
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
129 FTLRGTVVGSDSTSTHGAFALAFGIGTSEVEHVLAFOCLITRSKMRQVUGELAP 188
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
116 VTLPGMTVTCGSDSTHATHGAFALAFGIGTSEVEHVLAFOCLITRSKMRQVUGELAP 175
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
189 GVSASDVVLAIGITAGTAGVAVIEFGSVYRSISMERNISCNMSIEGARGAVNAPD 248
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
176 GIRAQDVLVLAIGTSGAGCGTHVFEFGDAIRALSMGKRTLCMALEMGAQGLVAPD 235
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
249 EITFEYKGRPLAKYDSPENHKAQYWKNLQSPGAKYDIDVFIADKDIYFTLTWGSTP 308
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
236 EITFENVYKGLHMK--GRPDEAVEVEYKTKTDGAFDFVTVTLRAEIIAPQVWTGNTP 293
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY EDVVPITGVVPDPEFATKAKAGRMLQYMGILKAGTPMEDIDIPDKYFIGCTNSRIED 368
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DB 294 GQVISTVDIIPDPASPSDVERASAEKALAVMGLQPGVPLTDVAIDKVFIGCTNSRIED 353
QY 369 LRAAAAVKGRKKAIPNVKAMVVPVGSGLVTKQAEEDGIDKIFEEAGFEWEGSCMCIQM 428
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DB 354 LRAAAVAKRKXKAPGVQ-ALVYPGSSPVYAAQAEABLDKIFIEAGFEWRLPGSMCIAM 412
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QY 429 NPDLAPQERCASTSRNPFEGROGAGGRTHTLMSGPVMMAAGIYVKLADVRL 480
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 413 NDRLNPRGECASSTSRNPFEGROGAGGRTHTLMSGPVMMAAAAVTGTFADIRSI 464
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
RESULT 24
LEU2_HAEIN
ID LEU2_HAEIN STANDARD; PRT; 468 AA.
AC P44968;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
DE (isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMT).
GN LEUC OR H10988.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
OC Haemophilus.
OC NCBI_TaxId=727;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Rd / KM20 / ATCC 51907;
RX MEDLINE=95350630; Pubmed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.U., Tomb J.-F., Dougherty B.A., Mierick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shrivley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Usterbach T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Funtmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd."
RL Science 269:496-512(1995).
CC -1- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
CC and 3-isopropylmalate, via the formation of 2-isopropylmalate.
CC -1- CATALYTIC ACTIVITY: 3-isopropylmalate = 2-isopropylmalate +
CC H(2)O.
CC -1- CATALYTIC ACTIVITY: 2-isopropylmalate + H(2)O = 2-
CC isopropylmalate.
CC -1- PATHWAY: Leucine biosynthesis; second step.
CC -1- SUBUNIT: Heterodimer of leuc and leud (By similarity).
CC -1- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY. LEUC 1
CC SUBFAMILY.
CC -----
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CC -----
CC EMBL; U32779; AAC22649.1; -
CC TIGR; H10988; -
CC InterPro: IPR001030; Aconitase_N.
CC InterPro: IPR004430; Leuc.
CC Pfam: PF00130; aconitase.1.
CC PRINTS; PR00415; ACONITASE.
CC PRODOM; PD000511; Aconitase_N.1.
CC TIGRFAMs; TIGR00170; leuc.1.
CC PROSITE; PS00450; ACONITASE_1; 1.
CC PROSITE; PS01244; ACONITASE_2; 1.
CC KW Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
CC FT INIT MET 0
CC METAL 346 346 IRON-SULFUR (4FE-4S) (BY SIMILARITY).

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FT METAL 407 407 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 410 410 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 SQ SEQUENCE 468 AA; 50743 MW; 0F6AFAP97AAAB9F6 CRC64;
 Query Match 36.3%; Score 1471; DB 1; Length 468;
 Best Local Similarity 59.4%; Pred. No. 4.7e-92;
 Matches 281; Conservative 72; Mismatches 112; Indels 8; Gaps 2;
 QY 9 QTLVQKVLQAHVDEKLDGTVLLYIDRLHVEVTSPOAFEGELRNAGKVRPDCATLTTD 68
 DB 2 KTLVQKVLQAHVDEKLDGTVLLYIDRLHVEVTSPOAFEGELRNAGKVRPDCATLTTD 61
 QY 69 HNVPTTSRKALKDIAFIKEDDSRTQCVTLLENVKEFGVTFYGLSKRQGIHVHVGPEQ 128
 DB 62 HSISTQVRDVK-----LEGOAKIQVLELDKNTKATGIKLPDITTEQGIHVHVGPEQ 115
 QY 129 FTLPGTIVCGDSHTSTHGAFAFGIGTSEVHVLAQTCLTKSKNMRIOVDGELAP 198
 DB 116 LTLPGMTIVCGDSHTATHGAFALAFGIGTSEVHVLAQTCLTKQARAKSMKIEVRGKVAS 175
 QY 189 GVSSKDVVLHAIGIITAGGTGAVIEFCGVSIRLSMEARMSICNMSIEGAGRVAPD 248
 DB 176 GITAKDIVLAIIGTGSAGGTGHVVFCEGEALRDLSEMGRTMLCNMAIEMGAKAGLVAPD 235
 QY 249 EITTEYLKGRPLAPKYDSPENHAKATQYKKNLOSQDPAKYDIDVFDADKIDVPLTLWTGSP 308
 DB 236 EITTEYLKGRPLAPKYDSPENHAKATQYKKNLOSQDPAKYDIDVFDADKIDVPLTLWTGSP 293
 QY 309 EDVPIITGVVDPPEATKADGRMLQYMGKAGTPEMEDIPVKVFGICSTNSRIED 368
 DB 294 QGVISVNDNIPDPASFPDVERSAEKALAYMGLKPGILLTVAIDKVFICSTNSRIED 353
 QY 369 LRAAAVVKGRKAPNVKSAWVPGSLVKTQAEELGDKIFEEAGPEWEAGCSMCLGM 428
 DB 354 LRAAAVVKGRKAPNVKSAWVPGSLVKTQAEELGDKIFEEAGPEWEAGCSMCLGM 412
 QY 429 NFDILAPORCASTSNRNFEGROGAGGRTHLMSFVMAAAAGIVGKLADVRKLT 481
 DB 414 NDRDLGEWERCASSTNRNFEGROGRNTHLVSPFAMAAAAGVFGKFDIRDVT 466
 RESULT 25
 LEU2 ECO57
 ID LEU2 ECO57 STANDARD; PRT; 465 AA.
 AC Q8XA00;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
 DE (isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
 GN LEUC OR 20081 OR ECS0076.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074335; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoudis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 RL Nature 409:529-533(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 CC -I- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
 and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
 CC -I- CATALYTIC ACTIVITY: 3-isopropylmaleate = 2-isopropylmaleate +
 H(2O).
 CC -I- CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2O) = 2-
 isopropylmaleate.
 CC -I- PATHWAY: Leucine biosynthesis; second step.
 CC -I- SUBUNIT: Heterodimer of leuc and leud (By similarity).
 CC -I- SIMILARITY: BELONGS TO THE ACNITASE/IPM ISOMERASE FAMILY. LEUC 1
 SUBFAMILY.
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 CC -----
 DR EMBL; AE005184; AAG54376.1; -.
 DR EMBL; AP002550; BAB33499.1; -.
 DR InterPro; IPR001030; Aconitase_N.
 DR InterPro; IPR004430; Leuc.
 DR Pfam; PF00330; aconitase; 1.
 DR PRINTS; PR00415; ACONITASE.
 DR ProDom; PD000511; Aconitase_N; 1.
 DR TIGRFAMs; TIGR00170; leuc; 1.
 DR PROSITE; PS00450; ACONITASE_1; 1.
 DR PROSITE; PS01244; ACONITASE_2; 1.
 KW Leucine biosynthesis; Lyase; Iron-sulfur; 4Fe-4S; Complete proteome.
 FT INIT MET 0
 FT METAL 346 346 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 406 406 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 409 409 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 SQ SEQUENCE 465 AA; 49766 MW; 72B977AE18AA2C41 CRC64;
 Query Match 36.2%; Score 1469.5; DB 1; Length 465;
 Best Local Similarity 61.9%; Pred. No. 5.9e-92;
 Matches 292; Conservative 59; Mismatches 112; Indels 9; Gaps 4;
 QY 9 QTLVQKVLQAHVDEKLDGTVLLYIDRLHVEVTSPOAFEGELRNAGKVRPDCATLTTD 68
 DB 2 KTLVQKVLQAHVDEKLDGTVLLYIDRLHVEVTSPOAFEGELRNAGKVRPDCATLTTD 61
 QY 69 HNVPTTSRKALKDIAFIKEDDSRTQCVTLLENVKEFGVTFYGLSKRQGIHVHVGPEQ 128
 DB 62 HNVSTQT---KDINAC--GEMARIQMOELINKCKEFGVELYDLNHPYQGIHVHVGPEQ 115
 QY 129 FTLPGTIVCGDSHTSTHGAFAFGIGTSEVHVLAQTCLTKSKNMRIOVDGELAP 198
 DB 116 VTLPGMTIVCGDSHTATHGAFALAFGIGTSEVHVLAQTCLTKQARAKTMKIEVQGAAP 175
 QY 189 GVSSKDVVLHAIGIITAGGTGAVIEFCGVSIRLSMEARMSICNMSIEGAGRVAPD 248
 DB 176 GITAKDIVLAIIGTGSAGGTGHVVFCEGEALRDLSEMGRTMLCNMAIEMGAKAGLVAPD 235
 QY 249 EITTEYLKGRPLAPKYDSPENHAKATQYKKNLOSQDPAKYDIDVFDADKIDVPLTLWTGSP 308
 DB 236 EITTEYLKGRPLAPKYDSPENHAKATQYKKNLOSQDPAKYDIDVFDADKIDVPLTLWTGSP 293
 QY 309 EDVPIITGVVDPPEATKADGRMLQYMGKAGTPEMEDIPVKVFGICSTNSRIED 368
 DB 294 QGVISVNDNIPDPASFPDVERSAEKALAYMGLKPGILLTVAIDKVFICSTNSRIED 353
 QY 369 LRAAAVVKGRKAPNVKSAWVPGSLVKTQAEELGDKIFEEAGPEWEAGCSMCLGM 428
 DB 354 LRAAAVVKGRKAPNVQVQ-ALVVPVPGSPVKAQAEAGLKDIFIEAGFEWRLPGSCMCLAM 412

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Oy 429 NPDILAPQRCASTSNRNFGRGAGGRTHIMSVMAAAAGIVGLADVRL 480
| | | | | : | | | | | : | | :
Db 413 NNDRLNGRCASITSNRNFGRGGRGRTHLVSPAAAAAVTGHFADIRNI 464

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Job time : 24 secs

